



CC inhibition of fertility. The present sequence represents the human sperm  
CC specific surface protein C58  
XX  
SQ Sequence 124 AA;

Query Match 100.0%; Score 684; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MVLGMLLLVMAALPGTTGKDCVFCGLTDSMOCPEGTTHHCGDDECFTHGVAPEGTPV 60  
1 MVLGMLLLVMAALPGTTGKDCVFCGLTDSMOCPEGTTHHCGDDECFTHGVAPEGTPV 60  
QY 61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
Db 61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
QY 121 PRL 124  
121 PRL 124  
Db 121 PRL 124

## RESULT 2

AA089146 standard; protein; 124 AA.

AC AAG89146;

DT 11-SEP-2001 (first entry)

DE Human secreted protein, SEQ ID NO: 266.

XX Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;

OS Homo sapiens.

XX MO200142451-A2.

PD 14-JUN-2001.

PF 07-DEC-2000; 2000MO-IB001938.

PR 08-DEC-1999; 99US-0169629P.

PR 06-MAR-2000; 2000US-0187470P.

PA (GENSET ) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S;

DR WPI; 2001-367870/38.

DR N-PSDB; AAH64749.

PT Full length GENSET human nucleic acids encoding potentially secreted  
PT proteins, useful in gene therapy and vaccination against a variety of  
PT diseases, and for diagnosis of those diseases.

PS Claim 21; Page 807; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding  
CC potentially secreted proteins. The nucleic acids and the polypeptides  
CC they encode may be used in the prevention, treatment and diagnosis of  
CC diseases associated with inappropriate GENSET gene expression. For  
CC example, they be used to treat disorders associated with decreased GENSET  
CC gene expression by rectifying mutations or deletions in a patient's  
CC genome that affect the activity of GENSET or by supplementing the  
CC patient's own production of GENSET polypeptides. Conversely, antisense  
CC nucleic acid molecules may be administered to down regulate GENSET  
CC expression by binding with the cells' own genes and preventing their  
CC expression. The sense and antisense nucleic acids may also be used as DNA  
CC probes in diagnostic assays to detect and quantitate the presence of  
CC similar nucleic acid sequences in samples, and hence to determine which  
CC patients may be in need of restorative therapy. The GENSET polypeptides

CC may be used as antigens in the production of antibodies and in assays to  
CC identify modulators (agonists and antagonists) of GENSET polypeptide  
CC expression and activity. The present sequence is a GENSET polypeptide of  
CC the invention  
XX

Query Match 100.0%; Score 684; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVLGMLLLVMAALPGTTGKDCVFCGLTDSMOCPEGTTHHCGDDECFTHGVAPEGTPV 60  
1 MVLGMLLLVMAALPGTTGKDCVFCGLTDSMOCPEGTTHHCGDDECFTHGVAPEGTPV 60  
Db 1 MVLGMLLLVMAALPGTTGKDCVFCGLTDSMOCPEGTTHHCGDDECFTHGVAPEGTPV 60  
QY 61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
Db 61 INKGLRATSCGLEBPVSRYGVYTSLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120  
QY 121 PRL 124  
121 PRL 124  
Db 121 PRL 124

## RESULT 3

AA083605 standard; protein; 124 AA.

AC AA083605;

DT 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 28.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

KW breast cancer; prostate tumour; rectal tumour; liver tumour;

KW pericyte cell proliferation; chondrocyte cell proliferation;

XX tumour necrosis factor-alpha.

OS Homo sapiens.

XX MO200208288-A2.

PD 31-JAN-2002.

PF 29-JUN-2001; 2001MO-US021066.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220585P.

PR 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.

PR 25-JUL-2000; 2000US-0220666P.

PR 26-JUL-2000; 2000US-0220893P.

PR 28-JUL-2000; 2000MO-US020710.

PR 28-JUL-2000; 2000MO-US022425P.

PR 22-AUG-2000; 2000MO-US027133P.

PR 23-AUG-2000; 2000MO-US023522.

PR 24-AUG-2000; 2000MO-US023528.

PR 10-NOV-2000; 2000MO-US030873.

PR 28-NOV-2000; 2000US-0253646P.

PR 01-DEC-2000; 2000MO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000MO-US034956.

PR 28-FEB-2001; 2001MO-US006520.

PR 01-MAR-2001; 2001MO-US006666.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001MO-US017092.

XX

XX (GENTH ) GENENTECH INC.  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
P1 Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,  
XX WPI; 2002-172001/22.  
DR N-PSDB; ABRK3549.  
XX  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumors such  
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor  
PT or liver tumor.  
XX  
XX  
PS Claim 11; Fig 28; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumors, especially lung  
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or  
CC liver tumor. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumor necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
CC protein sequences of the invention  
XX  
XX Sequence 124 AA;

Query Match	100.0%	Score 684	DB 5	length 124
Best Local Similarity	100.0%	Pred. No.	2.3e-54	
Matches 124	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

QY 1 MYLCMLLLNNVALPGTGTGVKDCVCECLDSDMQPCTVYHCGDDEBCFPGHGAAPGTGPV 60

Db 1 MYLCMLLLNNVALPGTGTGVKDCVCECLDSDMQPCTVYHCGDDEBCFPGHGAAPGTGPV 60

QY 61 INKGCLARTSCGLEBPVSYRGVYTSILTNCCGRLCNRPSSQTVGATTSILAIGLMLP 120

Db 61 INKGCLARTSCGLEBPVSYRGVYTSILTNCCGRLCNRPSSQTVGATTSILAIGLMLP 120

RESULT 4	
AAEI7451	
ID	AAEI7451 standard; protein, 124 AA.
XX	
AC	AAEI7451;
XX	
DT	22-APR-2002 (first entry)
XX	
DE	Human secreted protein, zuparl.
XX	
KM	Human; secreted protein, zuparl; inflammation; immunosuppressive; cancer;
KM	tissue remodelling; vaccine; autoimmune disease; cell-mediated immunity;
KM	fibrinolysis coagulation; circulatory anomaly; wound healing; vulnery;
KM	contraception; sperm motility; fertilisation; immuncontraceptive;
KM	spermatogenesis; antiinflammatory; contraceptive; antinfertility;
KM	gene therapy; chromosome 19q.13.32.

FT	Protein	20..124
FT	/label= Mature_human_zuparl_protein	
FT	Domain	20..110
FT	/note= "Extracellular domain"	
FT	Region	22..24
FT	/note= "Beta strand"	
FT	Disulfide-bond	23..47
FT	Disulfide-bond	25..34
FT	Region	38..40
FT	/note= "Beta strand"	
FT	Disulfide-bond	41..65
FT	Region	46..52
FT	/note= "Beta strand"	
FT	Region	60..66
FT	/note= "Beta strand"	
FT	Disulfide-bond	71..90
FT	Region	76..80
FT	/note= "Alpha helix"	
FT	Region	89..91
FT	/note= "Beta strand"	
FT	Disulfide-bond	91..95
FT	Domain	111..124
FT	/note= "Membrane associated domain"	
XX		
PN	WO200202636-A2.	
XX		
PD	10-JAN-2002.	
XX		
XX	02-JUL-2001; 2001WO-US021167.	
PF		
XX	30-JUN-2000; 2000US-0215446P.	
PR		
XX		
PA	(ZYMO ) ZYMOGENETICS INC.	
PI	Sheppard PO, Bishop PD, Presnell SR, Gilbert T;	
XX		
XX	WPI; 2002-154734/20.	
DR		
DR	N-PSDB; AAD28085.	
XX		
XX		
PT	Novel zuparl polypeptide useful for reducing inflammation, enhancing	
PT	viability of cryopreserved sperm, sperm motility, egg-sperm interactions,	
PT	and fertilization, or as components in antiinfertility vaccines.	
XX		
XX	Claim 1; Page 2; 94pp; English.	

FT	Query Match	Score	DB	Length
/label= Signal_peptide	100.0%	684	5	124

Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVLGMLLLVMAIPGTTGKDCVFCFLTDSMOCPGTYMHGDEDCFTGHGVAPEGVPV 60  
DB 1 MVLGMLLLVMAIPGTTGKDCVFCFLTDSMOCPGTYMHGDEDCFTGHGVAPEGVPV 60  
QY 61 INKGLRATSCGLEBPVSYRGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120  
DB 61 INKGLRATSCGLEBPVSYRGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120  
QY 121 PRL 124  
DB 121 PRL 124

RESULT 5  
AAU83232  
ID AAU83232 standard; protein; 124 AA.

AAU83232;  
AC  
XX  
XX  
DT 08-MAY-2002 (first entry)  
XX  
XX  
DE Novel secreted protein Z931828G2P.  
XX  
XX  
KM Protein secretion; mammalian secreted polypeptide; MSP.  
XX  
OS Homo sapiens.  
XX  
PN WO200202621-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 28-JUN-2001; 2001WO-US020638.  
XX  
PR 30-JUN-2000; 2000US-0215446P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sheppard PO, Presnell SR,  
XX  
DR WPI; 2002-147999/19.  
XX  
DR N-PSDB; ABK3147.  
XX  
PT Novel isolated mammalian secreted polypeptide useful in therapeutic and  
PT diagnostic methods, to direct secretion of other proteins of interest  
PT from host cell, as educational tools, and as laboratory practicum kits.  
XX  
XX  
PS Claim 12; Page 382-383; 397pp; English.

The invention describes an isolated mammalian secreted polypeptide (MSP)  
(I). (I) is useful to direct the secretion of other proteins of interest  
from a host cell, to monitor secretion of proteins, to degenerate  
sequences comprising all nucleotide sequences encoding a particular  
polypeptide, to screen for cell metabolism affecting receptors, for  
identifying new target receptors and drug design, for identifying, for  
protein purification, for determining the weight of expressed MSP  
polypeptides as a ratio to total protein expressed, for identifying  
peptide cleavage sites, for coupling amino and carboxy terminal tags, for  
amino acid sequence analysis, for monitoring biological activities of the  
protein in vitro and in vivo, and to teach analytical skills and as  
reagents for the study of cells, receptors, and other binding molecules.  
The polynucleotide is useful for radiation hybrid mapping, and somatic  
cell genetic technique developed for constructing high-resolution,  
contiguous maps of mammalian chromosomes. Reagents disclosed in the  
invention may be used to detect metabolic abnormalities characterized by  
over or under production of the protein. This is the amino acid sequence  
of a mammalian secreted polypeptide, described in the method of the  
invention

Sequence 124 AA;

Query Match 100.0%; Score 684; DB 5; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVLGMLLLVMAIPGTTGKDCVFCFLTDSMOCPGTYMHGDEDCFTGHGVAPEGVPV 60  
DB 1 MVLGMLLLVMAIPGTTGKDCVFCFLTDSMOCPGTYMHGDEDCFTGHGVAPEGVPV 60  
QY 61 INKGLRATSCGLEBPVSYRGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120  
DB 61 INKGLRATSCGLEBPVSYRGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120  
QY 121 PRL 124  
DB 121 PRL 124

RESULT 6  
ABU80752  
ID ABU80752 standard; protein; 124 AA.

ABU80752;  
AC  
XX  
XX  
DT 23-JUN-2003 (first entry)  
XX  
XX  
DE Human PRO polypeptide #14.  
XX  
XX  
KM Human; PRO polypeptide; secreted and transmembrane protein;  
XX anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003036635-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 28-AUG-2002; 2002US-00230163.  
XX  
PR 25-JUL-2000; 2000US-0220638P.  
XX  
PR 01-JUN-2001; 2001WO-US017800.  
XX  
PR 29-JUN-2001; 2001WO-US021066.  
XX  
PR 09-APR-2002; 2002US-00119480.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
DR WPI; 2003-342045/32.  
XX  
DR N-PSDB; ACA66854.  
XX  
XX

One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for the manufacture of a medicament for diagnosing or treating  
PT tumour.

Claim 11; Fig 28; 314pp; English.  
The present invention relates to the isolation of novel human PRO  
polypeptides, and the polynucleotide sequences encoding them. The PRO  
polypeptides are secreted and transmembrane proteins. The PRO  
polypeptides and polynucleotides are useful for preparing a medicament  
useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are  
useful in diagnostic assays for PRO, by detecting its expression in  
specific cells, tissues or serum, and for affinity purification of PRO  
from recombinant cell culture or natural sources. ABU80739-ABU80860  
represent the human PRO polypeptides of the invention. Note: The sequence  
data for this patent was obtained in electronic format directly from the  
USPTO web site at [seqdata.uspto.gov/patididEntry.html](http://seqdata.uspto.gov/patididEntry.html)

Sequence 124 AA;

Query Match 100.0%; Score 684; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLCWILLVMAIPPTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60  
 DB 1 MYLCWILLVMAIPPTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60

QY 61 INKGLRATSCGLEBPVSRYGVVYSLTTNCTGRLCNRA PSSQTVGATTSIALGLMLLP 120  
 DB 61 INKGLRATSCGLEBPVSRYGVVYSLTTNCTGRLCNRA PSSQTVGATTSIALGLMLLP 120

QY 121 PRL 124  
 DB 121 PRL 124

RESULT 7  
 ABO33718  
 ID ABO33718 standard; protein; 124 AA.

XX ABO33718;  
 XX  
 XX 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO9862.  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;  
 KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;  
 KW pharmaceutical; diagnostic; biosensor; bioresactor; tumour; lung tumour;  
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
 KW liver tumour; bone disorder; cartilage disorder; sports injury;  
 KW arthritis; wound.

XX Homo sapiens.  
 OS  
 XX US2003045687-A1.  
 XX  
 XX 06-MAR-2003.  
 PD  
 XX 12-AUG-2002; 2002US-00218631.  
 PF  
 XX 01-JUN-2001; 2001WO-US017800.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-APR-2002; 2002US-00119480.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 XX  
 XX WPI; 2003-512315/48.  
 DR N-PSDB; ACDB8606.  
 DR  
 XX  
 XX New genes, and its encoded secreted and transmembrane polypeptides,  
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or  
 PT pericyte proliferation, especially for treating lung tumors, arthritis or  
 PT wounds in a mammal.

XX Claim 11; Fig 28; 314PP; English.

XX The invention describes an isolated nucleic acid molecule comprising a  
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of  
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are  
 CC fully defined in the specification; or (b) any of 122 nucleotide  
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the  
 CC specification; or the full length coding sequence of any these 122  
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful  
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are  
 CC particularly useful for detecting tumors (e.g. lung tumour, colon  
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)  
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,  
 CC for stimulating the proliferation or differentiation of chondrocyte  
 CC cells, for stimulating proliferation of pericyte cells, or for modulating

CC normal human dermal fibroblast proliferation. The PRO nucleic acid or  
 CC polypeptide is also useful for treating tumors or various bone and/or  
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The  
 CC PRO polypeptides are useful in drug screening, particularly as targets  
 CC for therapeutic intervention in these diseases, and in the diagnostic  
 CC determination of the presence of these diseases. The PRO polypeptides are  
 CC also useful as molecular weight markers, or for chromosome  
 CC identification. The PRO genes are useful as hybridization probes, or for  
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may  
 CC also be used in gene therapy, particularly for replacing a defective  
 CC gene. This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide

XX Sequence 124 AA;

SO

Query Match 100.0%; Score 684; DB 6; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLCWILLVMAIPPTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60  
 DB 1 MYLCWILLVMAIPPTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60

QY 61 INKGLRATSCGLEBPVSRYGVVYSLTTNCTGRLCNRA PSSQTVGATTSIALGLMLLP 120  
 DB 61 INKGLRATSCGLEBPVSRYGVVYSLTTNCTGRLCNRA PSSQTVGATTSIALGLMLLP 120

QY 121 PRL 124  
 DB 121 PRL 124

RESULT 8  
 ABUS2061  
 ID ABUS2061 standard; protein; 124 AA.

XX ABUS2061;  
 XX  
 XX 25-JUN-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO9862.  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cardiac; cytosolic;  
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;  
 KW gene therapy; cardiovascular disorder; endothelial disorder;  
 KW angiotensin disorder; cardiac hypertrophy; tremor; cancer;  
 KW age-related macular degeneration; atherosclerosis; hypertension;  
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;  
 KW thrombophlebitis; lymphatic; tumour angiogenesis; breast carcinoma;  
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.  
 OS  
 XX US2003088063-A1.  
 XX  
 XX 08-MAY-2003.  
 PD  
 XX 12-AUG-2002; 2002US-00219003.  
 PF  
 XX 25-JUN-2000; 2000US-0220664P.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-APR-2002; 2002US-00119480.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 XX  
 XX WPI; 2003-393229/37.  
 DR N-PSDB; ACA68510.  
 DR  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides.

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
XX  
PS Claim 11; Fig 28; 314pp; English.  
XX  
CC The invention describes one hundred and eighty seven nucleic acids  
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The  
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for  
CC treating or diagnosing a cardiovascular, endothelial or angiogenic  
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-  
CC related macular degeneration, atherosclerosis, hypertension, arterial  
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,  
CC thrombolytic, lymphangitis, tumour angiogenesis (such as breast  
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids  
CC have applications in molecular biology, including use as hybridisation  
CC probes, and in chromosome and gene mapping. This is the amino acid  
CC sequence of a novel human secreted and transmembrane PRO polypeptide  
XX  
SQ Sequence 124 AA:  
  
Query Match 100.0%; Score 684; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MVLQWLLLVMAIPPTGTVKDCVFCELTDSMOCPTVMHCGDDECFTHGVAPGTGPV 60  
DB 1 MVLQWLLLVMAIPPTGTVKDCVFCELTDSMOCPTVMHCGDDECFTHGVAPGTGPV 60  
QY 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSLALGLMLLP 120  
DB 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSLALGLMLLP 120  
QY 121 PRLL 124  
DB 121 PRLL 124  
  
RESULT 9  
ABJ72241  
ID ABJ72241 standard; protein; 124 AA.  
XX  
AC ABJ72241;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human PRO9862 protein.  
XX  
KM PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;  
KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003050448-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 28-AUG-2002; 2002US-00230414.  
XX  
PR 01-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-APR-2002; 2002US-00119480.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
XX WPI; 2003-521818/49.  
XX  
XX N-PSDB; ABT44239.  
XX  
PT New nucleic acid encoding for a PRO protein, useful for the manufacture  
PT of a medicament for diagnosing or treating tumours or for measuring or  
PT detecting expression of an associated gene.

XX  
XX Claim 11; Fig 28; 315pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid encoding a fully  
CC defined PRO polypeptide. The molecules of the invention may be useful for  
CC stimulating proliferation or gene expression in pericyte cells or the  
CC release of TNF-alpha from human blood. Other possible uses include the  
CC stimulation or inhibition of chondrocyte proliferation or  
CC differentiation, the stimulation of human dermal fibroblast cell  
CC proliferation and the detection of the presence of a tumour within a  
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture  
CC of a medicament for diagnosing or treating a tumour within a mammal or  
CC for measuring or detecting the expression of an associated gene, as well  
CC as during gene therapy. The current sequence is that of the human PRO  
XX  
SQ Sequence 124 AA:  
  
Query Match 100.0%; Score 684; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MVLQWLLLVMAIPPTGTVKDCVFCELTDSMOCPTVMHCGDDECFTHGVAPGTGPV 60  
DB 1 MVLQWLLLVMAIPPTGTVKDCVFCELTDSMOCPTVMHCGDDECFTHGVAPGTGPV 60  
QY 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSLALGLMLLP 120  
DB 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSLALGLMLLP 120  
QY 121 PRLL 124  
DB 121 PRLL 124  
  
RESULT 10  
ABJ72369  
ID ABJ72369 standard; protein; 124 AA.  
XX  
AC ABJ72369;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human PRO9862 protein.  
XX  
KM PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;  
KW tumour necrosis factor; proliferation; differentiation; gene therapy;  
KW dermal fibroblast.  
XX  
OS Homo sapiens.  
XX  
PN US2003027988-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 26-AUG-2002; 2002US-00227884.  
XX  
PR 01-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-APR-2002; 2002US-00119480.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
XX  
XX WPI; 2003-503301/47.  
XX  
XX N-PSDB; ABT44522.  
XX  
PT New PRO protein encoding nucleic acid, useful for preparing PRO  
PT polypeptides and anti-PRO antibodies for detecting the presence of a  
PT tumor in a mammal.





XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for the manufacture of a medicament for diagnosing or treating  
PT tumor.  
PS Claim 11; Fig 28; 315pp; English.  
XX  
CC This invention relates to one hundred and twenty two novel nucleic acids  
CC encoding human PRO membrane bound proteins or receptors. Extracellular  
CC proteins play important roles in the formation, differentiation and  
CC maintenance of multicellular organisms. The fate of many individual cells  
CC (for example proliferation, migration or differentiation) is typically  
CC governed by information received from other cells and the immediate  
CC environment. The information is often transmitted by secreted  
CC polypeptides (for example mitogenic factors, survival factors, cytotoxic  
CC factors, differentiation factors, neuropeptides and hormones) which are  
CC received and interpreted by diverse cell receptors or membrane bound  
CC proteins. These membrane bound proteins and receptors may be of use as  
CC pharmaceutical and diagnostic agents, such as in the blocking of receptor  
CC -ligand interactions. The current invention provides the amino acid  
CC sequences of novel human membrane bound receptors and proteins, along  
CC with the cDNA sequences encoding them. The novel proteins of the  
CC invention may have cytosolic activities through the stimulation of  
CC chondrocytes. The nucleic acids of the invention may be useful for the  
CC manufacture of a medicament for diagnosing or treating a tumour in a  
CC mammal. In addition, they may be useful for measuring or detecting the  
CC expression of a tumour associated gene. The present sequence is the amino  
CC acid sequence of a human PRO protein of the invention  
SQ Sequence 124 AA;  
Query Match 100.0%; Score 684; DB 7; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYLCWLLLVMLPPTGTVKDCVFCELTDSMOCPCGTVMHCGDDEDCFTGHGVAPEGTV 60  
DB 1 MYLCWLLLVMLPPTGTVKDCVFCELTDSMOCPCGTVMHCGDDEDCFTGHGVAPEGTV 60  
QY 61 INKGLRATSCGLEBPVSRYGVTSLTNNCTGRLCNRASSQTVGATTSIALGLMLLP 120  
DB 61 INKGLRATSCGLEBPVSRYGVTSLTNNCTGRLCNRASSQTVGATTSIALGLMLLP 120  
QY 121 PRL 124  
DB 121 PRL 124  
QY 121 PRL 124  
DB 121 PRL 124  
RESULT 13  
ADB83518  
ID ADB83518 standard; protein; 124 AA.  
XX  
AC ADB83518;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO9862.  
XX  
KW human; secreted and transmembrane protein; PRO; cytosolic; vulnary;  
KW antitachytic; pericyte cell proliferation; chondrocyte cell proliferation;  
KW pericyte cell differentiation; chondrocyte cell proliferation;  
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;  
KW (TNF)-alpha release; dermal fibroblast cell proliferation;  
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;  
KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW liver tumour; tissue typing; chromosome mapping; gene mapping;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2003073814-A1.  
XX  
PD 17-APR-2003.

XX  
XX 12-AUG-2002; 2002US-00218849.  
PF  
XX  
XX 01-JUN-2001; 2001WO-US017800.  
PR  
XX 29-JUN-2001; 2001WO-US021066.  
PR  
XX 09-APR-2002; 2002US-00119480.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
PI WPI; 2003-644806/61.  
DR  
XX N-PSDB; ADB83517.  
DR  
XX  
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful  
PT in gene therapy, chromosome identification, tissue typing, or as  
PT hybridization probes in chromosome and gene mapping.  
PS Claim 11; Fig 28; 315pp; English.  
XX  
XX The invention describes an isolated PRO (secreted and transmembrane)  
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are  
CC useful for stimulating the proliferation of or gene expression in  
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful  
CC for stimulating the proliferation or differentiation of chondrocyte  
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide  
CC are useful for stimulating the release of tumour necrosis factor (TNF)-  
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,  
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,  
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,  
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,  
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,  
CC PRO1433, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567,  
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,  
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for  
CC stimulating the proliferation of normal human dermal fibroblasts cells.  
CC PRO181, PRO229, PRO788, PRO1194, PRO1488, PRO4302, PRO4408,  
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for  
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO  
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,  
CC are useful for detecting the presence of tumour in a mammal which  
CC involves comparing the level of expression of the above PRO polypeptides  
CC in a test sample of cells taken from the mammal, and a control sample of  
CC normal cells of the same cell type, where a higher level of expression of  
CC the PRO polypeptides in the test sample as compared to the control sample  
CC is indicative of the presence of tumour in the mammal. The tumour is lung  
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. (I) is useful as molecular weight markers, for tissue  
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is  
CC useful for chromosome and gene mapping or gene therapy. (II) is useful  
CC for generating transgenic animals or knock-out animals which are useful  
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide  
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,  
CC sport injuries). This is the amino acid sequence of a human secreted and  
CC transmembrane PRO polypeptide.  
XX  
SQ Sequence 124 AA;  
Query Match 100.0%; Score 684; DB 7; Length 124;  
Best Local Similarity 100.0%; Pred. No. 2.3e-54;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYLCWLLLVMLPPTGTVKDCVFCELTDSMOCPCGTVMHCGDDEDCFTGHGVAPEGTV 60  
DB 1 MYLCWLLLVMLPPTGTVKDCVFCELTDSMOCPCGTVMHCGDDEDCFTGHGVAPEGTV 60  
QY 61 INKGLRATSCGLEBPVSRYGVTSLTNNCTGRLCNRASSQTVGATTSIALGLMLLP 120  
DB 61 INKGLRATSCGLEBPVSRYGVTSLTNNCTGRLCNRASSQTVGATTSIALGLMLLP 120  
QY 121 PRL 124  
DB 121 PRL 124  
QY 121 PRL 124  
DB 121 PRL 124



Db 121 PRL 124

RESULT 14

ADB80624

ID ADB80624 standard; protein; 124 AA.

XX

AC ADB80624;

XX

DT 04-DEC-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO9862.

XX

KM Human; secreted and transmembrane protein; PRO; cytosolic; vulnery;

KM antiarthritic; pericyte cell proliferation;

KM pericyte cell differentiation; chondrocyte cell proliferation;

KM chondrocyte cell differentiation; tumour necrosis factor alpha release;

KM (TNF)-alpha release; dermal fibroblast cell proliferation;

KM dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

KM colon tumour; breast tumour; prostate tumour; rectal tumour;

KM liver tumour; tissue typing; chromosome mapping; gene mapping;

KM gene therapy.

XX

OS Homo sapiens.

XX

PN US2003088068-A1.

XX

PD 08-MAY-2003.

XX

PF 13-AUG-2002; 2002US-00219481.

XX

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX

XX (GETH ) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

DR WPI; 2003-657982/62.

DR N-PSDB; ADB80623.

XX

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,

PT useful in gene therapy, chromosome identification, tissue typing, or as

PT hybridization probes in chromosome and gene mapping.

XX

PS Claim 11, Fig 28; 305pp; English.

XX

CC The invention describes an isolated PRO (secreted and transmembrane)

CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

CC useful for stimulating the proliferation of or gene expression in

CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful

CC for stimulating the proliferation or differentiation of chondrocyte

CC cells. PRO231, PRO357, PRO125, PRO155, PRO1306 or PRO1419 polypeptide

CC are useful for stimulating the release of tumour necrosis factor (TNF)-

CC alpha from human blood. PRO982, PRO357, PRO723, PRO1306, PRO1419, PRO214,

CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,

CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,

CC PRO1025, PRO1186, PRO1126, PRO1186, PRO1272, PRO1244, PRO1412,

CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338,

CC PRO1443, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1360, PRO1567,

CC PRO1887, PRO1928, PRO3441, PRO1801, PRO4333, PRO3543, PRO3444, PRO3422,

CC PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for

CC stimulating the proliferation of normal human dermal fibroblasts cells.

CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,

CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for

CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO

CC polypeptides such as PRO6004, PRO4981, PRO1717, PRO5778, PRO4332, etc.,

CC are useful for detecting the presence of tumour in a mammal which

CC involves comparing the level of expression of the above PRO polypeptides

CC in a test sample of cells taken from the mammal, and a control sample of

CC normal cells of the same cell type, where a higher level of expression of

CC the PRO polypeptides in the test sample as compared to the control sample

CC is indicative of the presence of tumour in the mammal. The tumour is lung

CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or

CC liver tumour. (I) is useful as molecular weight markers, for tissue

CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is

CC useful for chromosome and gene mapping or gene therapy. (II) is useful

CC for generating transgenic animals or knock-out animals which are useful

CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide

CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,

CC sport injuries). This is the amino acid sequence of a human secreted and

CC transmembrane PRO polypeptide.

XX

XX Sequence 124 AA:

XX

SQ

Query Match 100.0%; Score 684; DB 7; Length 124;

Best Local Similarity 100.0%; Pred. No. 2.3e-54;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVLGMLLLVLMALPGTTGVKDCVFCFLTDSMQCPGTVMHCGDEDCFTGHGVAPTGPV 60

Db 1 MVLGMLLLVLMALPGTTGVKDCVFCFLTDSMQCPGTVMHCGDEDCFTGHGVAPTGPV 60

Qy 61 INKGLRATSCGLEBVSRYRGVTSITTNCTGRLCNRAPSSQTVGATSLALGLMLP 120

Db 61 INKGLRATSCGLEBVSRYRGVTSITTNCTGRLCNRAPSSQTVGATSLALGLMLP 120

Qy 121 PRL 124

Db 121 PRL 124

Db 121 PRL 124

RESULT 15

ADB73165

ID ADB73165 standard; protein; 124 AA.

XX

AC ADB73165;

XX

DT 04-DEC-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO9862.

XX

XX human; secreted and transmembrane protein; PRO; cytosolic; vulnery;

KM antiarthritic; pericyte cell proliferation;

KM pericyte cell differentiation; chondrocyte cell proliferation;

KM chondrocyte cell differentiation; tumour necrosis factor alpha release;

KM (TNF)-alpha release; dermal fibroblast cell proliferation;

KM dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

KM colon tumour; breast tumour; prostate tumour; rectal tumour;

KM liver tumour; tissue typing; chromosome mapping; gene mapping;

KM gene therapy.

XX

OS Homo sapiens.

XX

PN US2003096968-A1.

XX

PD 22-MAY-2003.

XX

PF 29-AUG-2002; 2002US-00232223.

XX

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX

XX (GETH ) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

DR WPI; 2003-765525/72.

DR N-PSDB; ADB73164.

XX

PT New isolated PRO polypeptides useful as molecular weight markers in

PT protein electrophoresis, useful for tissue typing, and for treating

PT arthritis and tumors.

PS Claim 11; Fig 28; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1129 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO211, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, CC PRO1478, PRO1114, PRO826, PRO365, PRO809, PRO1071, PRO1411, PRO1309, CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1274, PRO1412, CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338, CC PRO1343, PRO1376, PRO1387, PRO1405, PRO1474, PRO1317, PRO1760, PRO1657, CC PRO1940, PRO60798, PRO43341, PRO1801, PRO4333, PRO3343, PRO3444, PRO4332, CC stimulating the proliferation of normal human dermal fibroblasts cells. CC PRO181, PRO329, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., CC are useful for detecting the presence of tumour in a mammal which CC involves comparing the level of expression of the above PRO polypeptides CC in a test sample of cells taken from the mammal, and a control sample of CC normal cells of the same cell type, where a higher level of expression of CC the PRO polypeptides in the test sample as compared to the control sample CC is indicative of the presence of tumour in the mammal. The tumour is lung CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or CC liver tumour. (I) is useful as molecular weight markers, for tissue CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is CC useful for chromosome and gene mapping or gene therapy. (II) is useful CC for generating transgenic animals or knock-out animals which are useful CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide CC is useful for treating bone and/or cartilage disorders (e.g., arthritis, CC sport injuries). This is the amino acid sequence of a human secreted and CC transmembrane PRO polypeptide.

**SQ** Sequence 124 AA;

Query Match	100.0%	Score 684	DB 7	length 124
Best Local Similarity	100.0%	Pred. NC. 2.3e-54		
Matches 124	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

Search completed: April 15, 2005, 14:08:12  
Job time : 81 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 15, 2005, 14:00:50 ; Search time 184 Seconds

(without alignments)  
345.097 Million cell updates/sec

Title: US-10-809-654-16

Perfect score: 684

Sequence: 1 MVLGMLLLVLMALPGTTGV.....VGATSLALGLGMLPRILL 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	124	2	Q8TDM5
2	463	67.3	127	2	Q80ZD0
3	460	67.3	127	2	Q9DAK7
4	112.5	16.4	125	2	Q9JMP8
5	108	15.8	256	2	Q9D727
6	107.5	15.7	133	2	Q6M357
7	105	15.4	171	1	E323_MOUSE
8	104.5	15.3	111	2	Q9H2B5
9	104.5	15.3	240	1	IBP6_HUMAN
10	104	15.2	134	2	Q9D7B5
11	102.5	15.0	128	1	LY6D_HUMAN
12	102.5	15.0	382	2	Q9NZJ1
13	101	14.8	127	1	LY6D_MOUSE
14	99	14.5	171	1	E323_HUMAN
15	98.5	14.4	123	1	CD59_PIG
16	97	14.2	123	1	PSCA_HUMAN
17	96.5	14.1	118	1	LYNX_MACMU
18	95	13.9	189	2	Q9PM14
19	93	13.6	119	2	Q6UP92
20	92.5	13.5	129	2	Q9NCR0
21	92.5	13.5	153	1	NEUV_FUGRU
22	92.5	13.5	249	2	Q6PEX9
23	92	13.5	127	2	Q9DD23
24	92	13.5	135	2	Q9Z1Q3
25	91.5	13.4	133	2	Q9S6S8
26	91.5	13.4	134	2	Q6MGS8
27	90.5	13.2	125	2	Q6UXB3
28	90.5	13.2	208	2	Q96DR2
29	90.5	13.2	251	2	Q6UWN5
30	89.5	13.1	122	2	Q9NCR4
31	89.5	12.9	123	1	PSCA_MOUSE

32	87.5	12.8	118	2	Q9NCQ7	Q9NCQ7 dendroides
33	87	12.7	166	2	Q8KIT6	Q8KIT6 mus musculus
34	86.5	12.6	126	1	LY6E_CHICK	Q90866 gallus galli
35	86	12.6	294	2	Q9GVJ3	Q9GVJ3 caenorhabditis
36	86	12.6	346	2	Q9S274	Q9S274 mus musculus
37	86	12.6	346	2	Q9U074	Q9U074 homo sapien
38	85.5	12.5	560	2	Q9U013	Q9U013 giardia lam
39	85.5	12.5	966	2	Q22378	Q22378 caenorhabditis
40	84.5	12.4	123	2	Q9NCQ9	Q9NCQ9 dendroides
41	84.5	12.4	123	2	Q9D7U0	Q9D7U0 mus musculus
42	84.5	12.4	136	2	Q9NCR2	Q9NCR2 dendroides
43	84.5	12.4	474	2	Q6BEF1	Q6BEF1 mus musculus
44	84	12.3	119	2	Q64HX7	Q64HX7 oncorhynchus
45	84	12.3	201	2	Q9PRC7	Q9PRC7 oxytruncus m

## ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	124 AA.
Q8TDM5			
AC	Q8TDM5		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	28-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Speech acrosomal membrane protein 14 (SPACA4).		
GN	Name=SPACA4; Synonyms=SPACA4; ORFNames=UNG3046;		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=22791710; PubMed=12788941; DOI=10.1074/jbc.M301713200;		
RA	Shetty J., Wolkowicz M.J., Digilio L.C., Klotz K.L., Hayes P.L.,		
RA	Diekmann A.B., Westbrook V.A., Farris E.M., Hao Z., Coonrod S.A.,		
RA	Flickinger C.J., Herr J.C.;		
RT	"SAMP14, a novel, acrosomal membrane-associated,		
RT	glycosylphosphatidylinositol-anchored member of the Ly-6/urokinase-		
RT	type plasminogen activator receptor superfamily with a role in sperm-		
RT	egg interaction.";		
RL	J. Biol. Chem. 278:30506-30515(2003).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Bromstein M.J., Uedl T.B., Tohyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Lomellano N.A., Peters J.G., Abramson R.D., Mulhally S.J.,		
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.R., Hulik S.W.,		
RA	Villanar D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywnicki M.I., Skalska U., Smallos D.E., Schmeich A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RA	"Generation and initial analysis of more than 15,000 full-length human		
RA	and mouse cDNA sequences.";		
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Strausberg R.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		

[4]  
SEQUENCE FROM N.A.  
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurey A.L., Abaya E., Baker K., Baldwin D., Bush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Stammers L., Singh J., Smith V., Stinson J., Vagtes A.,  
RA Vandlen R., Watnabe C., Wleand D., Woods K., Xie M.H., Yanesa D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL/AF53721; AA183950.1; -;  
DR EMBL/BC047334; AA47334.1; -;  
DR EMBL/AY358387; AA08753.1; -;  
DR Gene/NCBI:16441; SPACA4.  
SQ SEQUENCE 124 AA; 13004 MW; 53407C5CCD8FC8BF CRC64;  
Query Match 100.0%; Score 684; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 7e-56; Mismatches 0; Gaps 0;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVLQMLLLVVALPPTGTVKDCVFCFLTDSMOCPGTYMHCGDDECFTHGVAFGTGPV 60  
DB 1 MVLQMLLLVVALPPTGTVKDCVFCFLTDSMOCPGTYMHCGDDECFTHGVAFGTGPV 60  
QY 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCTGRLCNRAPSSQTVGATTSALGLGLLP 120  
DB 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCTGRLCNRAPSSQTVGATTSALGLGLLP 120  
QY 121 PRLL 124  
DB 121 PRLL 124  
DB 121 PRLL 124

RESULT 2  
080Z00 PRELIMINARY; PRT; 127 AA.  
AC 080Z00;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE RIKEN CDNA 1700008E09.  
GN Name=1700008E09Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;  
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner J., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan K., Moore T., Max S.T., Wang J., Hsieh F.,  
RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarane P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywiński M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Maitra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL/BC048608; AA48608.1; -;  
DR MGI:1916613; 1700008E09Rik.  
SQ SEQUENCE 127 AA; 13380 MW; A4871BA47F8C41B6 CRC64;  
Query Match 67.7%; Score 463; DB 2; Length 127;  
Best Local Similarity 67.7%; Pred. No. 2.4e-35; Mismatches 25; Indels 2; Gaps 1;  
Matches 84; Conservative 13; Mismatches 25; Indels 2; Gaps 1;  
QY 1 MVLQMLLLVVALPPTGTVKDCVFCFLTDSMOCPGTYMHCGDDECFTHGVAFGTGPV 60  
DB 1 MVLQMLLLVVALPPTGTVKDCVFCFLTDSMOCPGTYMHCGDDECFTHGVAFGTGPV 60  
QY 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCTGRLCNRAPSSQTVGATTSALGLGLLP 120  
DB 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCTGRLCNRAPSSQTVGATTSALGLGLLP 120  
QY 121 PRLL 124  
DB 121 PRLL 124  
DB 119 LLLL 122

RESULT 3  
Q9DAK7 PRELIMINARY; PRT; 127 AA.  
AC Q9DAK7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:1700008E09 product:hypothetical protein, full insert  
DE sequence.  
GN Name=1700008E09Rik.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA The FANTOM Consortium;  
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

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RT 'prepare full-length cDNA libraries for rapid discovery of new genes.';
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishire T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yonega Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1175-1177(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanasaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaishizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK005760; BAB24224.1; -
RW MGD: MGI:191613; 1700008B09Rik.
KM Hypothetical protein.
SQ SEQUENCE 127 AA; 13408 MW; B3A02B5D58BC41B6 CRC64;

Query Match 67.3%; Score 460; DB 2; Length 127;
Best Local Similarity 66.9%; Pred. No. 4,5e-35;
Matches 83; Conservative 14; Mismatches 25; Indels 2; Gaps 1;

QY 1 MVLWLLLVLMALPGTTGKDCVFCELTDSMOCPEGYMHGCGDEDCFTGHGVAPEGPV 60
DB 1 MVLGMPFLLVLCVPGVTGIXDCVFCFCELTDSARCPGTHMKCGDEDCFTGHGVAQGVPI 60

QY 61 INKGCIRATSCGLEEPVSRYGVTYSLTTCCTGRLCNRAPSSQTVGATTSIALGLMLP 120
DB 61 INKGVHSTSCGLEEPISYGLTYSLTTCGSHLCNKGTLST--GATSLSLGLQLLIG 118

QY 121 PRL 124
DB 119 LLL 122

Db 119 LLL 122

RESULT 4
Q9UMP8 PRELIMINARY; PRT; 125 AA.
AC Q9UMP8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE G6e protein.
GN Name=G6e;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99316314; PubMed=10384126;
RA Ribas G., Neville M., Wixon J.L., Cheng J., Campbell R.D.;
RT "Genes encoding three new members of the leukocyte antigen 6
RT superfamily and a novel member of Ig superfamily, together with genes
RT encoding the regulatory nuclear chloride ion channel protein (hRNCC)
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RT and an N omega-N omega-dimethylarginine dimethylaminohydrolase
RT homologue, are found in a 30-kb segment of the MHC class III region.";
RL J. Immunol. 163:278-287(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22074936; PubMed=12079290; DOI=10.1006/geno.2002.6794;
RA Mallia M., Campbell R.D., Aguado B.;
RT "Transcriptional analysis of a novel cluster of Ly-6 family members in
RT the human and mouse major histocompatibility complex: five genes with
RT many splice forms.";
RL Genome Res. 10:113-123(2002).
DR EMBL: AL245419; CAB52193.1; -
RW MGD: MGI:13524 MW; C09252P9BA822926 CRC64;
SQ SEQUENCE 125 AA; 13524 MW; C09252P9BA822926 CRC64;

Query Match 16.4%; Score 112.5; DB 2; Length 125;
Best Local Similarity 31.9%; Pred. No. 0.0083;
Matches 38; Conservative 11; Mismatches 55; Indels 15; Gaps 5;

QY 1 MVLWLLLVLMALPGTTGKDCVFCELTDSMOCPEGYMHGCGDEDCFTGHGVAPEGPV 60
DB 11 LFLGALGLTMS---PARGRLRCYICGFT--KCHPVPTECRDDEAC---GISIGTS-- 59

QY 61 INKGCIRATSCGLEEPVSRYGVTYSLTTCCTGRLCNRAPSSQTVGATTSIALGLML 119
DB 60 -GRKSCRAQCPLPGYATYMLSHSYTLMHRCCEQDLGNIAASPOOL---TSLASLPLFV 114

RESULT 5
Q9D7Z7 PRELIMINARY; PRT; 256 AA.
AC Q9D7Z7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male stomach cDNA, RIKEN full-length enriched
DE library, clone:2210003103 product:weakly similar to METASTASIS-
DE ASSOCIATED GPI-ANCHORED PROTEIN.
GN Name=2210003103Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaishizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayaishizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
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RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro N., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "Riken integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1157-1771 (2000).
[6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Atakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RU EMBL: AK008654; BAB25810.1; -
DR MGD; MGI:1924192; 2210003103Rik.
DR InterPro; IPR001526; LY6_UPAR.
DR SMART; SM00134; LU; 1.
DR POSITIVE; PS00983; LY6_UPAR; UNKNOWN 1.
SQ SEQUENCE 256 AA; 27450 MW; D66B5762C8D767B CRC64;

Query Match 15.8%; Score 108; DB 2; Length 256;
Best Local Similarity 26.3%; Pred. No. 0.042;
Matches 40; Conservative 14; Mismatches 46; Indels 52; Gaps 8;

QY 12 ALPRTGVVDCV--FCEL-----TSMQCPRTY----- 38
DB 90 ALPPDYAVVAGCATDYNLSMKTHDALPNISQAPNPOTLSGTECVAGLTHPEDCPEKS 149
QY 39 --MHCGDDED-CFTGHS---VAPGTGVINKGCLR--ATSCGLEPVSRYGVYSLTTNC 90
DB 150 RRVQCHQDQACACGCGNRNMNIGNSVYVYRTICHRPSCCTMGTTSP---WTSIDLGVC 205
QY 91 CTGRLCNRAPSSQTVGATTSLALGLMLPPR 122
DB 206 CEGHLCNRASVTQILPCTWSSA-----PPR 230

RESULT 6
Q6MG57 PRELIMINARY; PRT; 133 AA.
AC 06MG57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lymphocyte antigen 6 complex, locus G6E.
GN Name=ly6g6e;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RX Pubmed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shina T.,
RA Inoko H., Leinrich H., Guenther E., Reinhardt R., Himmelbauer H.;
RT "The genomic sequence and comparative analysis of the rat major

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RT histocompatibility complex.";
RL Genome Res. 14:631-639 (2004).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RA Behm S., Borzym K., Gelling S., Gimel V., Heitmann K., Kojima A.,
RA Lang N., Leinrich S., Thiel J., Sonntag M., Hurt P., Himmelbauer H.,
RA Sudbrak R., Reinhardt R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX883045; CAE83989.1; -
SQ SEQUENCE 133 AA; 14635 MW; C60DD9EC77F64CB4 CRC64;

Query Match 15.7%; Score 107.5; DB 2; Length 133;
Best Local Similarity 31.2%; Pred. No. 0.026;
Matches 34; Conservative 9; Mismatches 49; Indels 17; Gaps 4;

QY 17 TTGVKCVCFELDSDNQCPQTVHCGDDDCFTGHGVAQGTGP-----YINKGLRATSC 71
DB 24 TRGRILHCTCSF--ARPCYFVLTECHDEVC-----GVSQTSQNDVIERKCLPRAC 77
QY 72 GLEPVSRYGVYSLTTNCCCTGRLCNRAPSSQTVGATTSLALGLMLP 120
DB 78 PILGHTTVMSRSYTLQHQCCEODLCNTAASQRRP-----SLPLMTLLP 120

RESULT 7
E323 MOUSE
ID E323 MOUSE STANDARD; PRT; 171 AA.
AC 08BP5;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Protein BPGP3023 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eye;
RX MEDLINE=22354683; Pubmed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaado I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Butt C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Kanapi A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Choithia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grifmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Seton M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymhew-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eye;

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RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins K.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smallue D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
 CC -----  
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL: AK053620; BAC35449.1; -  
 DR EMBL: BC070462; AA070462.1; -  
 DR MGD: MG1:2443848; E130115503Rik.  
 DR InterPro: IPR001526; Ly6\_UPAR.  
 DR SMART: SM00134; LU; 1.  
 KW SIGNAL.  
 FT SIGNAL. 1 22 By similarity.  
 FT CHAIN 23 171 Protein EPP3023.  
 FT DOMAIN 47 141 UPAR/Ly6.  
 FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).  
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 QY 3 LCVLLLL-----VMALPFGTT---GVKDCVFCF-LTDSMOC-----P 35  
 DB 7 LALLLLSLVADCLKAQSRDFVKKDITLHPSFTTPYGGFKFTCKKADNTECNRMAP 66  
 QY 36 GTYMHC-GDDEDCFTGHGV-APGTGPIVINKCLRATSC--GLPEPVSYRGVYSLTNC 90  
 DB 67 DLY--CPDRRYCYCTHTMTVEVNTSISVTRGVPILECLSTGCRDS-EHNG--YKICTSC 121  
 QY 91 CTGRLCN-RAPSSQT--VGATTS 110  
 DB 122 CEGNICNLPLPRMETATFATTS 144  
 RESULT 8  
 ID 09H2B5 PRELIMINARY; PRT; 111 AA.  
 AC 09H2B5;  
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Insulin-like growth factor binding protein 6 (Fragment).  
 GN Name=IGFBP6;  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
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 RX SEQUENCE FROM N.A.  
 RX MEDLINE=21167382; PubMed=11267670; DOI=10.1016/S0167-4781(01)00192-0;  
 RA Daillly Y.P., Zhou Y., Linhart T.A., Baylink D.J., Strong D.D.,  
 RT "Structure and characterization of the human insulin-like growth  
 RT factor binding protein (IGFBP)-6 promoter: identification of a  
 RT functional retinoid response element.";  
 RL Biochim. Biophys. Acta 1518:145-151(2001).  
 DR EMBL: AF297519; AAC37059.1; -  
 DR HSSP: P24593; IHS9.  
 DR GO: GO:0005576; C:extracellular; IEA.  
 DR GO: GO:0005520; P:insulin-like growth factor binding; IEA.  
 DR GO: GO:0001558; P:regulation of cell growth; IEA.  
 DR InterPro: IPR009030; Grow\_fac\_recept.  
 DR InterPro: IPR000867; Ins1\_gro\_fac\_pr.  
 DR Pfam: PF00219; IGFBP; 1.  
 DR SMART: SM00121; IB; 1.  
 DR NON TER 111 111.  
 SO SEQUENCE 111 AA; 11236 MW; 235F748AC3C7B946 CRC64;  
 Query Match 15.3%; Score 104.5; DB 2; Length 111;  
 Best Local Similarity 30.3%; Pred. No. 0.041;  
 Matches 37; Conservative 10; Mismatches 50; Indels 25; Gaps 6;  
 QY 3 LCVLLLLVMALPFGTTGVDCVFCFELTDSMOCGTYMHCSDRDCFTGHVAPGTGPVIN 62  
 DB 10 LLLLLALLLAAASFG-GALARCPCGGCGVQACCG--GCVBERD-----GGSFREGCAEA 60  
 QY 63 KGCILR-ATSCGLEPVSRYGVYSLTNCCTGRLCNRAPSSQVAGTTSIALGLMLP 120  
 DB 61 EGCLEAREGECGVYTF-----NCAPLQGH--PPKDEAPLRLALLRGRCCLP 106  
 QY 121 PR 122  
 DB 107 AR 108  
 RESULT 9  
 ID IBP6\_HUMAN STANDARD; PRT; 240 AA.  
 AC P24592; Q14492;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Insulin-like growth factor binding protein 6 precursor (IGFBP-6) (IBP-6) (IGF-binding protein 6).  
 DE Name=IGFBP6; Synonyms=IBP6;  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 RN RN SEQUENCE FROM N.A.  
 RC TISSUE=Osteosarcoma;  
 RX MEDLINE=91225006; PubMed=1709161;  
 RA Kleiter M.C., Maslarz F.R., Bauer D.M., Zapf J.,  
 RT "Identification and molecular cloning of two new 30-kDa insulin-like  
 RT growth factor binding proteins isolated from adult human serum.";  
 RL J. Biol. Chem. 266:9043-9049(1991).  
 RN [2]  
 RN RN SEQUENCE FROM N.A.  
 RX MEDLINE=99189142; PubMed=10087296;  
 RA Ehrenborg E., Zazzi H., Lagercrantz S., Grangviat M., Hillerbrand U.,  
 RA Allander S.V., Larsson C., Luthman H.,  
 RT "Characterization and chromosomal localization of the human insulin-  
 RT like growth factor-binding protein 6 gene.";  
 RL Mamm. Genome 10:376-380(1999).  
 RN [3]  
 RN RN SEQUENCE FROM N.A., AND VARIANTS GLY-128 AND GLN-217.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D.,



RA Schnackwitz W.S., Sherwood J.K., Witrak I.A., Mickenson D.A.;  
RT "NIHES-SNPs: environmental genome project, NIHES B51578, Department  
of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";  
RL Submitted (OCT-2003) to the EMBL/Genbank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RQ TISSUE=Pancreas;  
RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altshul S.F., Zeeberg B., Boerwinkle K.H., Schaefer C.F., Bat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish P.,  
Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
Sapota M., Soares M.B., Bonaldi M.P., Csaavant T.L., Schetz T.E.,  
Brownstein M.J., Usdin T.B., Toehlyukl S., Carninci P., Prange C.,  
Kana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Halysk S.W.,  
Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,  
Butterfield J.Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
Schnercher A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 2-240 FROM N.A.  
RQ TISSUE=Placenta;  
RX MEDLINE=92049376; PubMed=1793983;  
RA Shimazaki S., Gao L., Shimonaka M., Ling N.;  
RT "Isolation and molecular cloning of insulin-like growth factor-binding  
protein-6.";  
RL Mol. Endocrinol. 5:938-948(1991).  
RN [6]  
RP PARTIAL SEQUENCE OF 28-42.  
RX MEDLINE=9120735; PubMed=1850257;  
RA Andrews D.L., Birdnam R.S.;  
RT "A novel human insulin-like growth factor binding protein secreted by  
osteoblast-like cells.";  
RL Biochem. Biophys. Res. Commun. 176:213-218(1991).  
RN [7]  
RP PRELIMINARY SEQUENCE OF 28-42.  
RX TISSUE=Cerebrospinal fluid;  
RA MEDLINE=9000596; PubMed=2551732; DOI=10.1016/0014-5793(89)81101-9;  
RQ Roghani M., Hosseini P., Lepage P., Ballard A., Binoux M.;  
RT "Isolation from human cerebrospinal fluid of a new insulin-like growth  
factor-binding protein with a selective affinity for IGF-II.";  
RL FEBS Lett. 255:253-258(1989).  
RN [8]  
RP CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=88241382; PubMed=9572875; DOI=10.1021/jl1972894e;  
RA Neumann G.M., Marino J.A., Bach L.A.;  
RT "Identification of O-glycosylation sites and partial characterization  
of carbohydrate structure and disulfide linkages of human insulin-like  
growth factor binding protein 6.";  
RL Biochemistry 37:6572-6585(1998).  
RN [9]  
RP DISULFIDE BONDS.  
RX MEDLINE=99262603; PubMed=10329650; DOI=10.1074/jbc.274.21.14587;  
RA Neumann G.M., Bach L.A.;  
RT "The N-terminal disulfide linkages of human insulin-like growth  
factor-binding protein-6 (hIGFBP-6) and hIGFBP-1 are different as  
determined by mass spectrometry.";  
RL J. Biol. Chem. 274:14587-14594(1999).  
CC -I- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs  
and have been shown to either inhibit or stimulate the growth  
promoting effects of the IGFs on cell culture. They alter the  
interaction of IGFs with their cell surface receptors.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- PTM: O-linked glycans consist of hexose (probably Gal), N-

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CC acetylhexosamine (probably GalNAc) and sialic acid residues. Major glycoforms consist of 8-16 monosaccharides (by homology to IGFBP-6 expressed recombinantly in CHO cells).
CC -1- SIMILARITY: Contains 1 IGFBP domain.
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DR EMBL; M62402; AAB06187.1; -.
DR EMBL; AJ006952; CAA07346.1; -.
DR DR EMBL; AY443494; AAR05445.1; -.
DR DR EMBL; BC003507; AAH03507.1; -.
DR DR EMBL; BC005007; AAH05007.1; -.
DR DR EMBL; BC010162; AAH10162.1; -.
DR DR EMBL; BC011708; AAH11708.1; -.
DR EMBL; M69054; AAA88070.1; -.
DR PIR; A39842; A39842.
DR PIR; S05699; S05699.
DR HSSP; P24593; IBOE.
DR Genev; HGNC:5475; IGFBP6.
DR MIM; 146735; -.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR009168; IGFBP1-6.
DR InterPro; IPR008671; Insl_gro_fac_pr.
DR InterPro; IPR00716; Thyroglobulin_1.
DR Pfam; PF00219; IGFBP, 1.
DR Pfam; PF00086; Thyroglobulin_1; 1.
DR PIRSF; PIRSF001969; IGFBP1-6; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00222; TGF_BINDING; FALSE NEG.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW Direct protein sequencing; Glycoprotein; Growth factor binding; Polymorphism; Signal.
FT FT SIGNAL 1 24 Insulin-like growth factor binding protein 6
FT FT CHAIN 25 240 Thyroglobulin type-I.
FT FT DOMAIN 186 234
FT FT DISULFID 29 32
FT FT DISULFID 40 44
FT FT DISULFID 57 63
FT FT DISULFID 71 84
FT FT DISULFID 78 104
FT FT DISULFID 163 190
FT FT DISULFID 201 212
FT FT DISULFID 214 234
FT FT CARBOHYD 126 126 O-linked (HexNAc. . .) (By similarity).
FT FT CARBOHYD 144 144 O-linked (HexNAc. . .) (By similarity).
FT FT CARBOHYD 145 145 O-linked (HexNAc. . .) (By similarity).
FT FT CARBOHYD 146 146 O-linked (HexNAc. . .) (By similarity).
FT FT CARBOHYD 152 152 O-linked (HexNAc. . .) (By similarity).
FT FT VARIANT 128 128 R->G. /FTId=VAR_018932.
FT FT VARIANT 217 217 R->O. /FTId=VAR_018933.
FT FT VARIANT 236 236 T->P (in dBSNP:1053134). /FTId=VAR_011907.
FT FT CONFLICT 2 2 T->C (in Ref. 5).
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Query Match 15.3%; Score 104.5; DB 1; Length 240;
Best Local Similarity 30.3%; Pred. No. 0.084;
Matches 37; Conservative 10; Mismatches 50; Indels 25; Gaps 6;

3 LCWILLIWMALPGRTTGKVCVFCECLDSMQCGGTVMHGCDDBDCFTGHGVAGPTGPVIN 62
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Db 10 LLLLLLLAASPG-GALANCPGCGGVQAGCPG---GCVEED-----GGSPAGCAEA 60  
 QY KGLCR-ATSCGLEEPVSYRGVTSLTNNCTGRLCNRAPSSQTVGATSLALGMLP 120  
 Db 61 EGCIRREGCGCGVYTP-----NCAPIGCH-PPKDEAPRLALLRGRCCLP 106  
 QY 121 PR 122  
 Db 107 AR 108  
 RESULT 10  
 Q9D7E5 PRELIMINARY; PRT; 134 AA.  
 ID Q9D7E5  
 AC Q9D7E5  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
 library, clone:231001102 product:putative Ly-6 superfamily member,  
 full insert sequence (ly6g6e protein, isoform A).  
 GN Name=ly6g6e;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 Kono H., Akiyama U., Nishi K., Kikunishi T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 [6]  
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; TISSUE=Tongue;  
 RA Aachai J., Aizawa K., Akiuchi S., Akimura T., Arai A., Aono H.,  
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanazaki T., Hara A., Hayatsu N., Hiramoto K., Hiraka T., Hori F.,  
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=22074936; PubMed=12079290; DOI=10.1006/geno.2002.6794;  
 RA Maliya M., Campbell R.D., Aguado B.;  
 RT "Transcriptional analysis of a novel cluster of Ly-6 family members in  
 the human and mouse major histocompatibility complex: five genes with  
 RT many splice forms";  
 RL Genomics 80:113-123(2002).  
 DR EMBL: AK009303; BAB26204.1; -;  
 DR EMBL: AJ315550; CAC85546.1; -;  
 DR MGD: MGI:1917524; Ly6g6e.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.  
 DR InterPro: IPR000472; Activin\_receptor.  
 DR InterPro: IPR001526; Ly6\_UPAR.  
 DR Pfam: PF01064; Activin\_1recp.1.  
 DR SMART: SM00134; LV; 1.  
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 Query Match 15.2%; Score 104; DB 2; Length 134;  
 Best Local Similarity 31.0%; Pred. No. 0.055;  
 Matches 31; Conservative 7; Mismatches 42; Indels 20; Gaps 4;  
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 Db 15 GTTGLTTPARKGLRYTCSF--AKPCDPPRCRDEVC-----GVSVGTSEKEREVIE 68  
 QY 62 NKGCRLATSCGLEEPVSYRGVTSLTNNCTGRLCNRAP 101  
 Db 69 RKGCRLPACPLLGATVWSRSYSLRHCCEDLCNAAS 108  
 RESULT 11  
 LY6D HUMAN STANDARD; PRT; 128 AA.  
 ID LY6D HUMAN  
 AC Q14210; Q43783; O8TBD4; Q92933;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Lymphocyte antigen Ly-6D precursor (E48 antigen).  
 GN Name=LY6D; Synonyms=E48;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
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 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-33.  
 RX MEDLINE=95310346; PubMed=7790363; DOI=10.1083/jcb.129.6.1677;  
 RA Brakenhoff R.H., Gerretsen M., Knippels E.M.C., van Dijk M.,  
 RA van Esen H., Weghuis D.O., Sinke R.J., Snow G.B.,  
 RA van Dongen G.A.M.S.;  
 RT "The human E48 antigen, highly homologous to the murine Ly-6 antigen  
 THB, is a GPI-anchored molecule apparently involved in keratinocyte  
 RT cell-cell adhesion";  
 RL J. Cell Biol. 129:1677-1689(1995).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98031741; PubMed=9366413;  
 RA Brakenhoff R.H., van Dijk M., Rood-Knippels E.M.C., Snow G.B.;



LY6D\_MOUSE  
ID LY6D\_MOUSE STANDARD; PRT; 127 AA.  
AC P35459;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Lymphocyte antigen Ly-6D precursor (Thymocyte B cell antigen) (THB).  
GN Name=Ly6d; Synonyms=Ly6l, Thb;  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Thymocytes;  
RX MEDLINE=93017863; PubMed=1401899;  
RA Gumley T.P., McKenzie I.F., Kozak C.A., Sandrin M.S.;  
RT "Isolation and characterization of cDNA clones for the mouse thymocyte  
B cell antigen (THB).";  
RL J. Immunol. 149:2615-2618(1992).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Leukocyte;  
RX MEDLINE=95369850; PubMed=7642235;  
RA Gumley T.P., McKenzie I.F., Sandrin M.S.;  
RT "Sequence and structure of the mouse Thb gene.";  
RL Immunogenetics 42:221-224(1995).  
RN (3)  
RP SEQUENCE FROM N.A.  
RC STRAIN=EVB/N; TISSUE=Salivary gland;  
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
Altebach S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisch F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahney J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN (1)  
RP SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- TISSUE SPECIFICITY: Thymocytes and B cells.  
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL: X63782; CAA45317.1; -;  
DR EMBL: LA0419; AAA79249.1; ALT\_INIT.  
DR EMBL: BC025135; AAH25135.1; -;  
DR PIR: A46526; A46526.  
DR MGI: 96881; Ly6d.  
DR InterPro: IPR003632; Ly-6 CD59.  
DR InterPro: IPR001526; Ly6\_UPAR.  
DR Pfam: PFO0021; UPAR\_Ly6; 1.  
DR ProDom: PD003128; Ly-6\_CD59; 1.  
DR SMART: SM00134; LU; 1.

DR PROSITE: P500963; Ly6 UPAR; 1.  
KW Antigen; GPI-anchor; Lipoprotein; Membrane; Multigene family; Signal.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 98 Lymphocyte antigen Ly-6D.  
FT PROPE 99 127 Removed in mature form (Potential).  
FT DOMAIN 21 108 UPAR/Ly6.  
FT DISULFID 23 45 By similarity.  
FT DISULFID 26 32 By similarity.  
FT DISULFID 38 63 By similarity.  
FT DISULFID 67 86 By similarity.  
FT DISULFID 87 92 By similarity.  
FT LIPID 98 98 GPI-anchor amidated serine (Potential).  
SQ SEQUENCE 127 AA; 13395 MW; 0AF039B77D105917 CRC64;  
Query Match 14.8%; Score 101; DB 1; Length 127;  
Best Local Similarity 31.4%; Pred. No. 0.099;  
Matches 37; Conservative 12; Mismatches 55; Indels 14; Gaps 4;  
QY 6 LLLVVALPPTGTVGDCVFCBLTDSMCPGYTMGDEDECFTHGVAFGTGPVINKGC 65  
DB 6 LVLLVLAVALTSPAMALRGHVC--TNSANCKNPQVPSNPFCKTVTSVPLNGNLVRKGC 63  
QY 66 LRAATSCGLEPVSRYGVTYSLLTNCCTGRLCNR-----AP-----SSQVYGAATSLAL 113  
DB 64 --ANSTSDYSQQGHVSSGSESVYVCCOTDLCHERLVSAAFGHALLSSVTLGLATLSL 119  
RESULT 14  
E323\_HUMAN STANDARD; PRT; 171 AA.  
ID E323\_HUMAN  
AC Q86Y78;  
DT 25-JUN-2005 (Rel. 46, Created)  
DT 25-JAN-2005 (Rel. 46, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Protein EPG3023 precursor (UNQ3023/PRO9821).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC MEDLINE=22887296; PubMed=12975309; DOI=10.1101/97.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
Bacon D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,  
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
Lewin L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,  
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN (2)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
Altebach S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisch F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahney J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE OF 23-37.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RL Protein Sci. 13:2819-2824(2004).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
CC -----  
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CC -----  
DR EMBL: A358623; AA08986.1; -;  
DR EMBL: BC047013; AA47013.1; -;  
KW Direct protein sequencing; signal.  
FT SIGNAL 1 22  
FT CHAIN 23 171 Protein ERGP3023.  
FT DOMAIN 47 141 UPAR/Ly6.  
FT CARBOHYD 134 134 N-linked (GlcNAc.. ) (Potential).  
FT CARBOHYD 147 147 N-linked (GlcNAc.. ) (Potential).  
SQ SEQUENCE 171 AA; 19118 MW; 1BAEBE9CD18F5470 CRC64;  
Query Match 14.5%; Score 99; DB 1; Length 171;  
Best Local Similarity 25.3%; Pred. No. 0.2; Mismatches 49; Indels 58; Gaps 12;  
Matches 43; Conservative 20; Mismatches 49; Indels 58; Gaps 12;  
QY 3 LCMALL-----VMALPPTGTT--GVKDCVFCF-LTDSMQC-----P 35  
DB 7 LAMILLLSLLADCLKAQNSRDFVTKDIIYLHPSTTPYGGFKFCEKADNVECRMAP 66  
QY 36 GYTMHC-GGDEDFCTGHG-V-APGTGPVINKGCLRAISC--GLEBPVSRGVYSLTNC 90  
DB 67 DLY--CPRETRYCYTHMEVNTNSISVTKRCVPLEECISLTGRDS-EHGG--HKVCTSC 121  
QY 91 CTGRLCN-----RAPSSQTVG-----ATTSLALGKML 119  
DB 122 CEGNLCMLPLPRNETDATFTTSPINQTHGRPCMSVYISCLMWLGLML 171  
RESULT 15  
CD59\_PIG ID CD59\_PIG STANDARD; PRT; 123 AA.  
AC 062680; Q9TR76; Q9XT94;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE CD59 glycoprotein precursor (Membrane attack complex inhibition  
DE factor) (MACiP) (MAC-inhibitory protein) (MAC-iP) (Proectcin).  
GN Name=CD59;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.  
OC NCBI\_TaxID=9823;  
OC [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Aortic endothelium;  
RX MEDLINE=98217182; PubMed=9558099;  
RA Hinchliffe S.J., Rushmere N.K., Hanna S.M., Morgan B.P.;  
RT "Molecular cloning and xenotransplantation of the pig analogue  
RT of CD59: relevance to xenotransplantation.";  
RL J. Immunol. 160:3924-3932(1998).

RN [2]  
RP SEQUENCE OF 26-123 FROM N.A., AND FUNCTION.  
RC TISSUE=Aortic endothelium;  
RX MEDLINE=99023683; PubMed=9808497;  
RA Maher S.E., Pflugh D.L., Larsen N.J., Rothschild M.F.,  
RA Bothwell A.L.M.;  
RT "Structure/function characterization of porcine CD59: expression,  
RT chromosomal mapping, complement-inhibition, and costimulatory  
RT activity.";  
RL Transplantation 66:1094-1100(1998).  
RN [3]  
RP SEQUENCE OF 26-64.  
RC TISSUE=Erythrocyte;  
RX MEDLINE=95181826; PubMed=7533195; DOI=10.1016/0022-1759(94)00288-8;  
RA van den Berg C.W., Harrison R.A., Morgan B.P.;  
RT "A rapid method for the isolation of analogues of human CD59 by  
RT preparative SDS-PAGE: application to pig CD59.";  
RL J. Immunol. Methods 179:223-231(1995).  
CC -1- FUNCTION: Potent inhibitor of the complement membrane attack  
CC complex (MAC) action. Acts by binding to the C8 and/or C9  
CC complements of the assembling MAC, thereby preventing  
CC incorporation of the multiple copies of C9 required for complete  
CC formation of the osmolytic pore.  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested (lung, testis  
CC in liver, kidney, spleen, heart and skeletal muscle). Highest levels  
CC in lung and spleen, lowest levels in liver and skeletal muscle.  
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
CC -----  
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CC -----  
DR EMBL: AF020302; AAC67231.1; -;  
DR EMBL: AF058328; AAD39837.1; -;  
DR HSSP: P13987; 1ERG.  
DR InterPro: IPR003632; Ly-6 CD59.  
DR InterPro: IPR001526; Ly6 UPAR.  
DR Pfam: PFO0021; UPAR\_LY6\_1.  
DR ProDom: PDO03128; Ly-6-CD59; 1.  
DR SMART; SM00134; LU; 1.  
DR PROSITE; PS00983; Ly6 UPAR; 1.  
KW Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;  
KW Lipoprotein; signal.  
FT SIGNAL 1 25  
FT CHAIN 26 98  
FT PROPEP 99 123 CD59 glycoprotein.  
FT DOMAIN 26 103 Removed in mature form (By similarity).  
FT DISULFID 28 51 UPAR/Ly6.  
FT DISULFID 31 38 By similarity.  
FT DISULFID 44 65 By similarity.  
FT DISULFID 71 89 By similarity.  
FT DISULFID 90 95 By similarity.  
FT CARBOHYD 43 43 N-linked (GlcNAc.. ) (Potential).  
FT LIPID 98 98 GPI-anchor amidated serine.  
FT CONFLICT 26 26 L -> M (in Ref. 2).  
FT CONFLICT 46 46 H -> Y (in Ref. 3).  
FT CONFLICT 63 63 Missing (in Ref. 3).  
SQ SEQUENCE 123 AA; 13790 MW; FDE2ED3F93C91321 CRC64;  
Query Match 14.4%; Score 98.5; DB 1; Length 123;  
Best Local Similarity 27.0%; Pred. No. 0.16; Mismatches 47; Indels 27; Gaps 6;  
Matches 33; Conservative 15; Mismatches 47; Indels 27; Gaps 6;  
QY 2 VLCLMLLVMALPPTGVKDCVFCFELTDSMQC-----PG-----TYMGGDED--CFTHG 51  
DB 8 ILMLLSL-----AVLCHLGHSLGTCVNCINAGSCTTAMNCSSHQDACPVE 55  
QY 52 GVAPGTGPVINKGCLRAISCGLLEBPVSRGVYSLTNCCTGRLCNRAPSSQTVGATLSL 111

Mon Apr 18 12:46:39 2005

us-10-809-654-16.rup

**Page 11**

Db 56 AVEPKT---YYQWRPEECNDFP-!SNLAEKKLKTNCCKDKJCNKSDATISSGTALL 110  
Qy 112 AL 113  
Db 111 VI 112

Search completed: April 15, 2005, 14:04:11  
Job time : 193 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:00:50 ; Search time 16 Seconds

(without alignments)  
745.680 Million cell updates/sec

Title: US-10-809-654-16

Perfect score: 684  
Sequence: 1 MVLGMLLLVMAIPGTTGV.....VGATTSIALGLGMLPPRL 124

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: PIR 79:\*\*

1: p1r1:\*\*  
2: p1r2:\*\*  
3: p1r3:\*\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104.5	15.3	240	2 A39842	insulin-like growth
2	102.5	15.0	128	1 A57321	B48 antigen precursor
3	101	14.8	127	1 A46528	phosphatidylinositol
4	101	14.8	130	2 I54553	gene Thb protein -
5	85.5	12.5	1101	2 T16840	hypothetical prote
6	84	12.3	240	2 T25641	hypothetical prote
7	82.5	12.1	4543	1 A53102	alpha-2-macroglobu
8	80.5	11.8	222	2 B41643	urokinase-type pla
9	80.5	11.8	222	2 B55356	urokinase-type pla
10	80.5	11.8	327	2 A55356	urokinase-type pla
11	80.5	11.8	330	1 JN0561	urokinase-type pla
12	80.5	11.8	1111	2 T26972	hypothetical prote
13	80.5	11.8	1381	2 T20406	hypothetical prote
14	78.5	11.5	1620	2 T27283	hypothetical prote
15	78	11.4	328	2 S42152	urinary plasminoge
16	77.5	11.4	509	2 I59576	transforming growth
17	77.5	11.3	516	2 A48678	activin receptor I
18	77.5	11.3	685	2 JCT570	delta-4 protein -
19	77	11.3	61	1 N1N3E	short neurotoxin 3
20	77	11.3	312	2 T31834	hypothetical prote
21	77	11.3	503	2 A49432	activin receptor-1
22	77	11.3	513	2 S28358	presore vesicle p
23	76	11.1	83	2 S19951	neurotoxin-like pe
24	76	11.1	5376	2 T42215	zonadhesin - mouse
25	75.5	11.0	128	1 RWH59	surface glycoprote
26	75.5	11.0	2160	2 T29764	hypothetical prote
27	75	11.0	61	1 N1N04E	short neurotoxin 4
28	75	11.0	134	2 I48639	neurotoxin homolog
29	75	11.0	509	2 A45992	activin A receptor

30	74	10.8	122	2 PN0622	insulin-like growth
31	74	10.8	136	2 I49013	chymic shared anti
32	74	10.8	248	2 T31841	hypothetical prote
33	74	10.8	509	2 A49664	activin type I rec
34	73.5	10.7	81	2 S27366	metallothionein E
35	73.5	10.7	158	2 B34132	vasotocin / neurop
36	73	10.7	161	2 A46189	vasotocin - Pacifi
37	72.5	10.6	82	2 JC5892	cobrotoxin b - Chi
38	72.5	10.6	134	2 A25708	ly-6.1 protein pre
39	72.5	10.6	603	2 S28941	coagulation factor
40	72.5	10.6	1252	2 S36016	oocyte wall protei
41	72	10.5	249	2 T31837	hypothetical prote
42	72	10.5	496	2 T41114	urotophyrin methy
43	71.5	10.5	153	2 A34132	vasotocin / neurop
44	71.5	10.5	559	1 A29941	c-plasminogen acti
45	71.5	10.5	1321	2 JE0352	mucin MUC5B, trach

#### ALIGNMENTS

RESULT 1  
A39842  
insulin-like growth factor-binding protein 6 precursor - human  
N/Alternate names: IGFBP-6, insulin-like growth factor II-binding protein  
C/Species: Homo sapiens (man)  
C/Date: 20-Mar-1992 #sequence revision 31-Dec-1995 #text\_change 09-Jul-2004  
R/Accession: A39842; B23734; PH0144; A35470; C35803  
R/Kleier, M.C.; Maslitz, F.R.; Bauer, D.M.; Zapf, J.  
J. Biol. Chem. 265, 9043-9049, 1991  
A/Title: Identification and molecular cloning of two new 30-kDa insulin-like growth factor  
A/Reference number: A39842; NCID:91225006; PMID:1709161  
A/Accession: A39842  
A/Molecule type: mRNA  
A/Residues: 1-240 <KIE>  
A/Cross-references: UNIPROT:P24592; GB:M62402; NCID:9184813; PIDN:AAB06187.1; PID:G184814  
R/Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.  
Mol. Endocrinol. 5, 938-948, 1991  
A/Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6.  
A/Reference number: A23734; NCID:92049376; PMID:1719383  
A/Accession: B23734  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 'C', 3-240 <SHI>  
A/Cross-references: GB:M69054; NCID:9183893; PIDN:AAA08070.1; PID:9183894  
R/Andress, D.L.; Birnbaum, R.S.  
Biochem. Biophys. Res. Commun. 176, 213-218, 1991  
A/Experimental source: cell line V-2  
R/Martin, J.L.; Willette, K.E.; Baxter, R.C.  
J. Biol. Chem. 265, 4124-4130, 1990  
A/Title: Purification and properties of a novel insulin-like growth factor-II binding pr  
A/Reference number: A35470; NCID:90154107; PMID:2154495  
A/Accession: A35470  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 28, 'A', 30-39 <MAR>  
R/Zapf, J.; Kleier, M.; Merryweather, J.; Maslitz, F.; Bauer, D.; Born, W.; Fischer, J.A.  
J. Biol. Chem. 265, 14892-14898, 1990  
A/Title: Isolation from adult human serum of four insulin-like growth factor (IGF) bindin  
A/Reference number: A35803; NCID:90368661; PMID:1697583  
A/Accession: C35803  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 'AA', 30-31, 'H', 33-54, 'QXG' <ZAP>  
C/Genetics:  
A/Genes: GDB:IGFBP6  
A/Cross-references: GDB:127456; OMIM:146735



## RESULT 5

T16840 hypothetical protein T10E10.4 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T16840

Submitted to the EMBL Data Library, October 1995

A/Description: The sequence of *C. elegans* cosmid T10E10.

A/Reference number: Z18588

A/Accession: T16840

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1101 &lt;GEI&gt;

A/Cross-references: UNIPROT:Q22378; EMBL:U039644; NID:G1049339; PID:G1049343; PIDN:AAA803

A/Experimental source: strain Bristol N2

C/Genetics:

A:Gene: CESP.T10E10.4

A:introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match

Best Local Similarity 12.5%; Score 85.5; DB 2; Length 1101;

Matches 37; Conservative 21; Mismatches 37; Indels 49; Gaps 10;

Db

15 PGTGVDGCVFCELTDSMQ-----CPGTVM---HCGDDEDCFTGHGVAEGTG- 58

392 PGTGOCNKVCCQOTDTLNNLIQHQAICPGSNVPEPLGSC--NEGCPQYSACTRLGCG 449

59 -PV-INK---GCLRATSGLEEVSYRGVYSLTNCCTGRLCN-----RAPSSQ 103

Db

450 CPVAVNEQPGMKITKILC-----PGSY-SPFVGCGSCPSCTGQCNQQLQMCPCPLQDPSTD 504

104 TV-----GATSLALGIG 116

Db

505 IVYVNVLLCPDPTTSCSKGCG 528

## RESULT 6

T25641 hypothetical protein C46H11.7 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T25641

Submitted to the EMBL Data Library, February 1997

A/Description: The sequence of *C. elegans* cosmid C46H11.

A/Reference number: Z20061

A/Accession: T25641

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-240 &lt;MIL&gt;

A/Cross-references: UNIPROT:Q0GY4; EMBL:U08314; PIDN:ABA42361.1; GSPDB:GN00019; CESP:C4

A/Experimental source: strain Bristol N2; clone C46H11

C/Genetics:

A:Gene: CESP.C46H11.7

A:introns: 26/1; 51/1; 195/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F48G7.8

Query Match

Best Local Similarity 12.3%; Score 84; DB 2; Length 240;

Matches 32; Conservative 10; Mismatches 42; Indels 22; Gaps 6;

Db

17 TTGVCDC---VCELTLD-----SMOCPEYVHCGDDEDCFTGHG--VAPGTPVINKG 64

Db

95 STGVSCDPCALAYLCNPTTYTYVTWQCCPRTGCRKNCSTTSSSCADLVNPSGTG--VSDC 152

Qy

65 CRRATSGGLEEVSYRGVYSLTNCCTGRLCNRAPSSQVAGMTS 110

Db

153 TAAASLCN-----DSVYAVMTQCCP-RTGCRKNCSSSTVTSSSS 190

RESULT 7

## A53102

alpha-2-macroglobulin receptor precursor - chicken

N/Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor

C/Species: *Gallus gallus* (chicken)

C/Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 09-Jul-2004

C/Accession: A53102

Submitted to the EMBL Data Library, October 1998

A/Description: The sequence of chicken cDNA clone pCD91, which encodes the alpha-2-macroglobulin receptor precursor.

A/Reference number: A53102; PMID:94103212; PMID:7506255

A/Accession: A53102

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-4543 &lt;NIM&gt;

A/Cross-references: UNIPROT:P98157; GB:X74904; NID:G438006; PIDN:CAA52870.1; PID:G438007

C/Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated

d protein.

C/Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C/Keywords: beta-hydroxyaspartic acid; beta-hydroxyaspartic acid; calcium binding; glycoprotein

F/1-17/Domain: signal sequence #status predicted &lt;SIG&gt;

F/18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted &lt;515K&gt;

F/18-3942.3943-4543/Product: alpha-2-macroglobulin receptor #status predicted &lt;MAT&gt;

F/28-66/Domain: LDL receptor ligand-binding repeat homology &lt;LDL1&gt;

F/74-110/Domain: LDL receptor ligand-binding repeat homology &lt;LDL2&gt;

F/117-150/Domain: EGF homology &lt;EG1&gt;

F/156-190/Domain: EGF homology &lt;EG2&gt;

F/200-241/Domain: LDL receptor YWTD-containing repeat homology &lt;YW01&gt;

F/242-283/Domain: LDL receptor YWTD-containing repeat homology &lt;YW02&gt;

F/284-336/Domain: LDL receptor YWTD-containing repeat homology &lt;YW03&gt;

F/337-380/Domain: LDL receptor YWTD-containing repeat homology &lt;YW04&gt;

F/381-422/Domain: LDL receptor YWTD-containing repeat homology &lt;YW05&gt;

F/423-470/Domain: LDL receptor YWTD-containing repeat homology &lt;YW06&gt;

F/480-521/Domain: EGF homology &lt;EG3&gt;

F/573-615/Domain: LDL receptor YWTD-containing repeat homology &lt;YW07&gt;

F/616-661/Domain: LDL receptor YWTD-containing repeat homology &lt;YW08&gt;

F/662-712/Domain: LDL receptor YWTD-containing repeat homology &lt;YW09&gt;

F/713-754/Domain: LDL receptor YWTD-containing repeat homology &lt;YW10&gt;

F/755-797/Domain: LDL receptor YWTD-containing repeat homology &lt;YW11&gt;

F/805-840/Domain: EGF homology &lt;EG4&gt;

F/852-888/Domain: LDL receptor ligand-binding repeat homology &lt;LDL3&gt;

F/893-929/Domain: LDL receptor ligand-binding repeat homology &lt;LDL4&gt;

F/934-969/Domain: LDL receptor ligand-binding repeat homology &lt;LDL5&gt;

F/974-1009/Domain: LDL receptor ligand-binding repeat homology &lt;LDL6&gt;

F/1013-1049/Domain: LDL receptor ligand-binding repeat homology &lt;LDL7&gt;

F/1060-1095/Domain: LDL receptor ligand-binding repeat homology &lt;LDL8&gt;

F/1102-1138/Domain: LDL receptor ligand-binding repeat homology &lt;LDL9&gt;

F/1143-1180/Domain: LDL receptor ligand-binding repeat homology &lt;LDL10&gt;

F/1183-1219/Domain: EGF homology &lt;EG5&gt;

F/1225-1259/Domain: EGF homology &lt;EG6&gt;

F/1267-1306/Domain: LDL receptor YWTD-containing repeat homology &lt;YW12&gt;

F/1307-1353/Domain: LDL receptor YWTD-containing repeat homology &lt;YW13&gt;

F/1354-1396/Domain: LDL receptor YWTD-containing repeat homology &lt;YW14&gt;

F/1397-1443/Domain: LDL receptor YWTD-containing repeat homology &lt;YW15&gt;

F/1444-1486/Domain: LDL receptor YWTD-containing repeat homology &lt;YW16&gt;

F/1487-1529/Domain: LDL receptor YWTD-containing repeat homology &lt;YW17&gt;

F/1538-1576/Domain: EGF homology &lt;EG7&gt;

F/1581-1624/Domain: LDL receptor YWTD-containing repeat homology &lt;YW18&gt;

F/1625-1667/Domain: LDL receptor YWTD-containing repeat homology &lt;YW19&gt;

F/1668-1711/Domain: LDL receptor YWTD-containing repeat homology &lt;YW20&gt;

F/1712-1751/Domain: LDL receptor YWTD-containing repeat homology &lt;YW21&gt;

F/1752-1794/Domain: LDL receptor YWTD-containing repeat homology &lt;YW22&gt;

F/1795-1842/Domain: LDL receptor YWTD-containing repeat homology &lt;YW23&gt;

F/1846-1882/Domain: EGF homology &lt;EG8&gt;

F/1930-1972/Domain: LDL receptor YWTD-containing repeat homology &lt;YW24&gt;

F/1973-2015/Domain: LDL receptor YWTD-containing repeat homology &lt;YW25&gt;

F/2016-2059/Domain: LDL receptor YWTD-containing repeat homology &lt;YW26&gt;

F/2060-2101/Domain: LDL receptor YWTD-containing repeat homology &lt;YW27&gt;

F/2102-2147/Domain: LDL receptor YWTD-containing repeat homology &lt;YW28&gt;

F/2155-2190/Domain: EGF homology &lt;EG9&gt;

F/2195-2237/Domain: LDL receptor YWTD-containing repeat homology &lt;YW29&gt;

F/2247-2288/Domain: LDL receptor YWTD-containing repeat homology &lt;YW30&gt;

F/2338-2382/Domain: LDL receptor YWTD-containing repeat homology &lt;YW31&gt;

F/2383-2423/Domain: LDL receptor YWTD-containing repeat homology &lt;YW32&gt;

F:2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>  
F:2476-2511/Domain: EGF homology <EG10>  
F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDLB>  
F:2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDLC>  
F:2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDLD>  
F:2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDLE>  
F:2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDLF>  
F:2732-2767/Domain: LDL receptor ligand-binding repeat homology <LDLG>  
F:2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDLH>  
F:2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDLI>  
F:2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDLJ>  
F:2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDLK>  
F:2941-2977/Domain: EGF homology <EG11>  
F:2983-3018/Domain: EGF homology <EG12>  
F:3026-3065/Domain: LDL receptor YWTD-containing repeat homology <YW35>  
F:3066-3110/Domain: LDL receptor YWTD-containing repeat homology <YW36>  
F:3111-3153/Domain: LDL receptor YWTD-containing repeat homology <YW37>  
F:3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW38>  
F:3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW39>  
F:3239-3281/Domain: LDL receptor YWTD-containing repeat homology <EG13>  
F:3291-3337/Domain: EGF homology <EG14>  
F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL>  
F:3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDLM>  
F:3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDLN>  
F:3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDLO>  
F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDLP>  
F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDLQ>  
F:3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDLR>  
F:3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDLS>  
F:3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDLT>  
F:3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLV>  
F:3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLW>  
F:3783-3820/Domain: EGF homology <EG15>  
F:3826-3858/Domain: EGF homology <EG16>  
F:3866-3899/Domain: LDL receptor YWTD-containing repeat homology <YW40>  
F:3910-3948/Domain: LDL receptor YWTD-containing repeat homology <YW41>  
F:3943-4011/Domain: alpha-2-macroglobulin receptor 85k chain #status predicted <85k>  
F:3943-4011/Domain: 85k chain extracellular #status predicted <EXT>  
F:3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>  
F:4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>  
F:4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>  
F:4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>  
F:4150-4181/Domain: EGF homology <EG17>  
F:4199-4230/Domain: EGF homology <EG18>  
F:4235-4266/Domain: EGF homology <EG19>  
F:4271-4302/Domain: EGF homology <EG20>  
F:4307-4338/Domain: EGF homology <EG21>  
F:4343-4373/Domain: EGF homology <EG22>  
F:4376-4408/Domain: EGF homology <EG23>  
F:4421-4443/Domain: transmembrane #status predicted <TM>  
F:4444-4533/Domain: intracellular #status predicted <INT>  
F:116-138,187,276,359,448,731,926,1048,1152,1153,1193,1305,1509,1556,1573,1614,1643,3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carboxyrate (Asn) (covalent)  
F:168/2995/Modified site: erythro-beta-hydroxyaspartate (Asp) #status predicted  
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 12.1%; Score 82.5; DB 1; Length 4543;  
Best Local Similarity 32.4%; Pred. No. 34;

Matches 24; Conservative 4; Mismatches 23; Indels 23; Gaps 4;

QY 19 GYKDC-----VFCELT-----TDSMQCPGYM-----HCGDEDCFTGHGVAAGTGPVI 61  
DB 2753 GADDCDGDSDSDSRCLTTCSTGTSFGCPGYVCVPRRWLCDGDKDC-----ADGADETL 2806  
QY 62 NKGLRATSCGLEE 75  
DB 2807 AAGCLYNTCTDRE 2820

RESULT 8  
B41643  
urokinase-type plasminogen activator receptor 2 - mouse  
C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #ext\_change 09-Jul-2004  
C:Accession: B41643  
R:Kristensen, P.; Eriksen, J.; Blasj, F.; Dano, K.  
J. Cell Biol. 115, 1763-1771, 1991  
A:Title: Two alternatively spliced mouse urokinase receptor mRNAs with different histologic  
A:Reference number: A41643; MUID:92098587; PMID:161735  
A:Accession: B41643  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-222 <KRI>  
A:Cross-references: UNIPROT:P35457; GB:X62701; NID:g53277; PID:CA44575.1; PID:g53278  
F:24-108/Domain: Ly-6 homology <LY6>

Query Match 11.8%; Score 80.5; DB 2; Length 222;  
Best Local Similarity 28.7%; Pred. No. 4.1;

Matches 31; Conservative 10; Mismatches 42; Indels 25; Gaps 5;

QY 3 LCMILLVWALPPGTGVDCVFCELTDSMQCPGYTMHCGDDEDCFTGHGVAAGT----- 58  
DB 7 LLLILLATTCVPASGGLD-CMQCESNQCIV-----EECALGDLCRTTVLREW 55  
QY 59 -----PVINKGLRATSCGLEEPVSYR--GVYSLTTNCTGRLCNR 98  
DB 56 QDDRELEVTVRG--AHSEKTRMTSYRMSITSLTEVCATNLNR 101

#### RESULT 9

B55356  
urokinase-type plasminogen activator receptor, hypothetical soluble form precursor - mou

C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #ext\_change 09-Jul-2004  
C:Accession: B55356

R:Sun, T.T.; Naylor, C.; Dano, K.; Degen, J.L.  
J. Biol. Chem. 269, 25992-25998, 1994

A:Title: The murine urokinase-type plasminogen activator receptor gene.  
A:Reference number: A55356; MUID:95014420; PMID:7929309

A:Accession: B55356

A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-222 <SNH>  
A:Cross-references: UNIPROT:Q91214; GB:U12235

A:Note: authors translated the codon TTG for residue 219 as Phe  
C:Genetics:  
A:introns: 20/1; 57/1; 105/1

C:Keywords: alternative splicing; duplication  
F:24-108/Domain: Ly-6 homology <LY6>

Query Match 11.8%; Score 80.5; DB 2; Length 222;  
Best Local Similarity 28.7%; Pred. No. 4.1;

Matches 31; Conservative 10; Mismatches 42; Indels 25; Gaps 5;

QY 3 LCMILLVWALPPGTGVDCVFCELTDSMQCPGYTMHCGDDEDCFTGHGVAAGT----- 58  
DB 7 LLLILLATTCVPASGGLD-CMQCESNQCIV-----EECALGDLCRTTVLREW 55  
QY 59 -----PVINKGLRATSCGLEEPVSYR--GVYSLTTNCTGRLCNR 98  
DB 56 QDDRELEVTVRG--AHSEKTRMTSYRMSITSLTEVCATNLNR 101

#### RESULT 10

A55356  
urokinase-type plasminogen activator receptor membrane form precursor - mouse

N:Alternate names: urokinase-type plasminogen activator receptor 1  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #ext\_change 09-Jul-2004  
C:Accession: A55356; A41643

R:Sun, T.T.; Naylor, C.; Dano, K.; Degen, J.L.  
J. Biol. Chem. 269, 25992-25998, 1994

A:Title: The murine urokinase-type plasminogen activator receptor gene.  
A:Reference number: A55356; MUID:95014420; PMID:7929309

A:Accession: A55356

A:Molecule type: DNA

```

Query Match      11.8%; Score 80.5; DB 1; Length 330;
Best Local Similarity 27.6%; Pred. No. 5.7;
Matches 29; Conservative 11; Mismatches 40; Indels 25; Gaps 5;

Oy      6 LLLLVMLPPEPTGVKQCVFCELTDSMOCPEVTYHAGCGDDECFGHHVAPOT----- 57
|||||  ||:::||::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||

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	Query Match	Similarity	11.8%	Score	80.5;	DB 2:	Length	1391;	
	Best Local	Similarity	24.3%	Pred.	No. 19;				
	Matches	Conservative	28;	Mismatches	48;	Indels	25;	Gaps	5
Qy	17	TTGVKDCVFCFELTDSMOCP-----GTYMHC-GDEDECFTGHGAVPGTGVPINKCCL	66						
	:	:::::							
Db	818	STGGAYC--CINTNVIRCPSSGSYFYBGXGRRLACPAGSNKKRPPGYSCHSPINPQHILCCS	875						
Qy	67	RATSCGLEEPPVSRYGVTV-----SLTNCTGTGLCNRA-PSSQTVGAT	108						
	:	:   ::							
Db	876	SGSGMGVSYQPQCULRGVAVYNPATNQRPFCSPMKADCPAGYTCFESDQSDFICCT	930						

